



#24

Atty Dkt. No.: 23001481

USSN: 09/297,648

CERTIFICATE OF MAILING			
I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Assistant Commissioner for Patents, Washington, D.C. 20231.			
Typed or Printed Name	Steven F. Goldstein		
Signature	<i>St F Goldstein</i>	Date	April 11, 2002
DECLARATION OF FILIPPO M. RANDAZZO AND GEORGE F. LAMSON UNDER 37 C.F.R. § 1.132 Address to: Assistant Commissioner for Patents Washington, D.C. 20231		Attorney Docket	23001481
		First Named Inventor	Williams et al.
		Application Number	09/297,648
		Filing Date	March 10, 2000
		Group Art Unit	1631
		Examiner Name	J. Brusca
		Title: <i>Novel Human Genes and Gene Expression Products II</i>	

Dear Sir:

1. I, Filippo M. Randazzo, declare and say I am a resident of the State of California. My residence address is 104 Capricorn Avenue, Oakland, CA 94611.
2. I hold a B.S. degree in Molecular Microbiology and Anthropology, which I received from the University of Notre Dame in 1985. I further hold a Ph.D. degree, which I received from Indiana University in 1991. I am skilled in the fields of genetics, molecular biology, developmental biology genomics and cancer biology. I am a co-inventor of the invention claimed in the above-referenced patent application.
3. I, George F. Lamson, declare and say I am a resident of the State of California. My residence address is 232 Sandringham Dr., Moraga, CA 94556.
4. I hold a BS degree in Biochemistry, which I received from the University of CA, Santa Barbara in 1976. I further hold a PhD degree, which I received from University of CA, Berkeley,

Exhibit 1

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in 1982. I am skilled in the fields of Bioinformatics. I am a co-inventor of the invention claimed in the above-referenced patent application.

5. I have reviewed the relevant portions of the Office Action (specifically section nos. 6 and 10), mailed October 2, 2001, in the above-referenced application. I understand that claims 58, 60-66, 116, and 126 of the above-referenced patent application are rejected under 35 U.S.C. §101 on the grounds that the claimed invention lacks patentable utility, and also under 35 U.S.C. §112, ¶ 1, on the grounds that since the claimed invention is not supported by a patentable utility, one skilled in the art would not know how to use the claimed invention.
6. This Declaration provides further evidence of the patentable utility of the claimed invention. Specifically, this Declaration provides evidence that the nucleotide sequence designated SEQ ID NO: 1186 represents genes that are differentially expressed in cancer cells, thus supporting the assertion that the claimed invention has utility in detecting cancer cells.
7. The following experiments were conducted by me or under my direction.
8. Genes differentially expressed in cancerous cells were identified as detected by microarray hybridization analysis using materials obtained from patient colon tissue samples. The biological materials used in these experiments, the methods of analysis, and the results are described below.
9. **Source of patient tissue samples.** Normal and cancerous tissues were collected from patients using laser capture microdissection (LCM) techniques, which techniques are well known in the art. **Table 1** (Attachment 1) provides information about each patient from which the samples were isolated, including: the Patient ID ("PT ID") and Path ReportID ("Path ID"), which are numbers assigned to the patient and the pathology reports for identification purposes; the group ("Grp") to which the patients have been assigned; the anatomical location of the tumor ("Anatom Loc"); the primary tumor size ("Size"); the primary tumor grade ("Grade"); the identification of

the histopathological grade ("Histo Grade"); a description of local sites to which the tumor had invaded ("Local Invasion"); the presence of lymph node metastases ("Lymph Met"); the incidence of lymph node metastases (provided as a number of lymph nodes positive for metastasis over the number of lymph nodes examined) ("Lymph Met Incid"); the regional lymphnode grade ("Reg Lymph Grade"); the identification or detection of metastases to sites distant to the tumor and their location ("Dist Met & Loc"); the grade of distant metastasis ("Dist Met Grade"); and general comments about the patient or the tumor ("Comments"). Histopathology of all primary tumors indicated the tumor was adenocarcinoma except for Patient ID Nos. 130 (for which no information was provided), 392 (in which greater than 50% of the cells were mucinous carcinoma), and 784 (adenosquamous carcinoma). Extranodal extensions were described in three patients, Patient ID Nos. 784, 789, and 791. Lymphovascular invasion was described in Patient ID Nos. 128, 228, 278, 517, 534, 784, 786, 789, 791, 890, and 892. Crohn's-like infiltrates were described in seven patients, Patient ID Nos. 52, 264, 268, 392, 393, 784, and 791.

10. **Source of polynucleotides on arrays.** Polynucleotides spotted on the arrays were generated by PCR amplification of clones derived from cDNA libraries. The clones used for amplification were either the clones from which the sequences described herein were derived, or are clones having inserts with significant polynucleotide sequence overlap with the sequences described herein as determined by BLAST2 homology searching.
11. **Microarray Design.** Each array used in the examples below had an identical spatial layout and control spot set. Each microarray was divided into two areas, each area having an array with, on each half, twelve groupings of 32 x 12 spots for a total of about 9,216 spots on each array. The two areas are spotted identically which provide for at least two duplicates of each clone per array. Spotting was accomplished using PCR amplified products from 0.5kb to 2.0 kb and spotted using a Molecular Dynamics Gen III spotter according to the manufacturer's recommendations. The first row of each of the 24 regions on the array had about 32 control spots, including 4 negative control spots and 8 test polynucleotides. The test polynucleotides

were spiked into each sample before the labeling reaction with a range of concentrations from 2-600 pg/slide and ratios of 1:1. For each array design, two slides were hybridized with the test samples reverse-labeled in the labeling reaction. This provided for about 4 duplicate measurements for each clone, two of one color and two of the other, for each sample.

12. **Microarray Analysis.** cDNA probes were prepared from total RNA isolated from the patient cells described in **Table 1** (Attachment 1). Since LCM provides for the isolation of specific cell types to provide a substantially homogenous cell sample, this provided for a similarly pure RNA sample. Total RNA was first reverse transcribed into cDNA using a primer containing a T7 RNA polymerase promoter, followed by second strand DNA synthesis. cDNA was then transcribed *in vitro* to produce antisense RNA using the T7 promoter-mediated expression, and the antisense RNA was then converted into cDNA. The second set of cDNAs were again transcribed *in vitro*, using the T7 promoter, to provide antisense RNA. Optionally, the RNA was again converted into cDNA, allowing for up to a third round of T7-mediated amplification to produce more antisense RNA. Thus the procedure provided for two or three rounds of *in vitro* transcription to produce the final RNA used for fluorescent labeling. Fluorescent probes were generated by first adding control RNA to the antisense RNA mix, and producing fluorescently labeled cDNA from the RNA starting material. Fluorescently labeled cDNAs prepared from the tumor RNA sample were compared to fluorescently labeled cDNAs prepared from normal cell RNA sample. For example, the cDNA probes from the normal cells were labeled with Cy3 fluorescent dye (green) and the cDNA probes prepared from the tumor cells were labeled with Cy5 fluorescent dye (red).

13. The differential expression assay was performed by mixing equal amounts of probes from tumor cells and normal cells of the same patient ("matched") or from tumor cells and normal cells of different patients ("unmatched") (*i.e.*, the tumor cells are from one patient and the normal cells are from a different patient). The arrays were prehybridized by incubation for about 2 hrs at 60°C in 5X SSC/0.2% SDS/1 mM EDTA, and then washed three times in water and twice in isopropanol. Following prehybridization of the array, the probe mixture was then hybridized to

the array under conditions of high stringency (overnight at 42°C in 50% formamide, 5X SSC, and 0.2% SDS. After hybridization, the array was washed at 55°C three times as follows: 1) first wash in 1X SSC/0.2% SDS; 2) second wash in 0.1X SSC/0.2% SDS; and 3) third wash in 0.1X SSC. The arrays were then scanned for green and red fluorescence using a Molecular Dynamics Generation III dual color laser-scanner/detector. The images were processed using BioDiscovery Autogene software, and the data from each scan set normalized to provide for a ratio of expression relative to normal. Data from the microarray experiments was analyzed according to the algorithms described in U.S. application serial no. 60/252,358, filed November 20, 2000, by E.J. Moler, M.A. Boyle, and F.M. Randazzo, and entitled "Precision and accuracy in cDNA microarray data." The experiment was repeated, this time labeling the two probes with the opposite color in order to perform the assay in both "color directions." Each experiment was sometimes repeated with two more slides (one in each color direction). The level fluorescence for each sequence on the array expressed as a ratio of the geometric mean of 8 replicate spots/genes from the four arrays or 4 replicate spots/gene from 2 arrays or some other permutation. The data were normalized using the spiked positive controls present in each duplicated area, and the precision of this normalization was included in the final determination of the significance of each differential. The fluorescent intensity of each spot was also compared to the negative controls in each duplicated area to determine which spots detected significant expression levels in each sample.

14. A statistical analysis of the fluorescent intensities was applied to each set of duplicate spots to assess the precision and significance of each differential measurement, resulting in a p-value testing the null hypothesis that there is no differential in the expression level between the tumor and normal samples of each patient. For initial analysis of the microarrays, the hypothesis was accepted if $p > 10^{-3}$, and the differential ratio was set to 1.000 for those spots. All other spots have a significant difference in expression between the tumor and normal sample. If the tumor sample has detectable expression and the normal does not, the ratio is truncated at 1000 since the value for expression in the normal sample would be zero, and the ratio would not be a mathematically useful value (e.g., infinity). If the normal sample has detectable expression and

the tumor does not, the ratio is truncated to 0.001, since the value for expression in the tumor sample would be zero and the ratio would not be a mathematically useful value. These latter two situations are referred to herein as "on/off." Database tables were populated using a 95% confidence level ($p > 0.05$).

15. In general, a polynucleotide is said to represent a significantly differentially expressed gene between two samples when there is detectable levels of expression in at least one sample and the ratio value is greater than at least about 1.2 fold, preferably greater than at least about 1.5 fold, more preferably greater than at least about 2 fold, where the ratio value is calculated using the method described above. A differential expression ratio of 1 indicates that the expression level of the gene in the tumor cell was not statistically different from expression of that gene in normal colon cells of the same patient. A differential expression ratio significantly greater than 1 in cancerous colon cells relative to normal colon cells indicates that the gene is increased in expression in cancerous cells relative to normal cells, indicating that the gene plays a role in the development of the cancerous phenotype, and may be involved in promoting metastasis of the cell.

16. **Table 2**, shown below, summarizes the results of the differential expression analysis in colon tissue. The table provides: (1) the SEQ ID NO of the polynucleotide corresponding to the polynucleotide on the spot on the array; (2) the Clone Name; (3) whether the tumor cells and normal cells were from the same patient ("matched") or were from different patients ("unmatched"); (4) the number of patients tested ("No. Tested"); (5) the percentage of patients tested in which detected expression level was greater than or equal to a 2-fold increase in cancerous tissue relative to normal tissue (" $\geq 2x$ "); (6) the percentage of patients tested in which detected expression level was greater than or equal to a 5-fold increase in cancerous tissue relative to normal tissue (" $\geq 5x$ "); and (7) the percentage of patients tested in which detected expression level was less than or equal to $\frac{1}{2}$ of the expression level in normal cells (" $\leq 0.5x$ ").

TABLE 2

SEQ ID NO:	Clone Name	Matched/ Unmatched	No. Tested	$\geq 2x$ 95% conf.	$\geq 5x$ 95% conf.	$\leq 0.5x$ 95% conf.
1186	M00032614C:B10	matched	40	67.5	12.5	48.48
1186	M00032614C:B10	unmatched	28	42.9	0.0	3.6

17. The data above support the assertion that a polynucleotide having a sequence of SEQ ID NO: 1186 represents genes that are differentially expressed in cancer cells, thus supporting the assertion that the claimed invention has utility in detecting cancer cells. Specifically, detection of gene products that correspond to genes having a sequence of SEQ ID NO: 1186 can provide an indicator that the cell is cancerous, and may provide a therapeutic and/or diagnostic target.

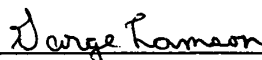
18. I, Filippo M. Randazzo, hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title XVIII of the United States Code, and that such will false statements may jeopardize the validity of the application or any patent issuing thereon.

3/28/02
Date


Filippo M. Randazzo

19. I, George Lamson, hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title XVIII of the United States Code, and that such will false statements may jeopardize the validity of the application or any patent issuing thereon.

3/28/02
Date


George Lamson

Attachments: Table 1 of patient data

F:\DOCUMENT\2300\1481\Declaration of Randazzo-Lamson for SEQ ID NO 1186.doc

Attachment 1

Table 1

Atty Dkt. No.: 23001481
 USSN: 09/297,648

Pt ID	Path ID	Grp	Anatom Loc	Size	Grade	Histo Grade	Local Invasion	Lymph Met	Lymph Met Incid	Reg Lymph Grade	Dist Met & Loc	Dist Met Grade	Comment
15	21	III	Ascending colon	4.0	T3	G2	Extending into subserosal adipose tissue	Pos	3/8	N1	Neg	MX	invasive adenocarcinoma, moderately differentiated; focal perineural invasion is seen
52	71	II	Cecum	9.0	T3	G3	Invasion through muscularis propria, subserosal involvement; ileocecal valve involvement	Neg	0/12	N0	Neg	M0	Hyperplastic polyp in appendix.
121	140	II	Sigmoid	6	T4	G2	Invasion of muscularis propria into serosa, involving submucosa of urinary bladder	Neg	0/34	N0	Neg	M0	Perineural invasion; donut anastomosis Neg. One tubulovillous adenoma with no high grade dysplasia.
125	144	II	Cecum	6	T3	G2	Invasion through the muscularis propria into subserosal adipose tissue. Ileocecal junction.	Neg	0/19	N0	Neg	M0	patient history of metastatic melanoma
128	147	III	Transverse colon	5.0	T3	G2	Invasion of muscularis propria into pericolonic fat	Pos	1/5	N1	Neg	M0	

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Pt ID	Path ID	Grp	Anatom Loc	Size	Grade	Histo Grade	Local Invasion	Lymph Met	Lymph Met Incld	Reg Lymph Grade	Dist Met & Loc	Dist Met Grade	Comment
130	149		Splenic flexure	5.5	T3		through wall and into surrounding adipose tissue	Pos	10/24	N2	Neg	M1	
133	152	II	Rectum	5.0	T3	G2	Invasion through muscularis propria into non-peritonealized pericolic tissue; gross configuration is annular.	Neg	0/9	N0	Neg	M0	Small separate tubular adenoma (0.4 cm)
141	160	IV	Cecum	5.5	T3	G2	Invasion of muscularis propria into pericolic adipose tissue, but not through serosa. Arising from tubular adenoma.	Pos	7/21	N2	Pos - Liver	M1	Perineural invasion identified adjacent to metastatic adenocarcinoma.
156	175	III	Hepatic flexure	3.8	T3	G2	Invasion through muscularis propria into subserosa/pericolic adipose, no serosal involvement. Gross configuration annular.	Pos	2/13	N1	Neg	M0	Separate tubulovillous and tubular adenomas

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Pt ID	Path ID	Grp	Anatom Loc	Size	Grade	Histo Grade	Local Invasion	Lymph Met	Lymph Met Incid	Reg Lymph Grade	Dist Met & Loc	Dist Met Grade	Comment
228	247	III	Rectum	5.8	T3	G2 to G3	Invasion through muscularis propria to involve subserosal, perirectal adipose, and serosa	Pos	1/8	N1	Neg	MX	Hyperplastic polyps
264	283	II	Ascending colon	5.5	T3	G2	Invasion through muscularis propria into subserosal adipose tissue.	Neg	0/10	N0	Neg	M0	Tubulovillous adenoma with high grade dysplasia
266	285	III	Transverse colon	9	T3	G2	Invades through muscularis propria to involve pericolic adipose, extends to serosa.	Neg	0/15	N1	Pos - Mesenteric deposit	MX	
267	286	III	Ileocecal	4.5	T2	G2	Confined to muscularis propria	Pos	2/12	N1	Neg	M0	
268	287	I	Cecum	6.5	T2	G2	Invades full thickness of muscularis propria, but mesenteric adipose free of malignancy	Neg	0/12	N0	Neg	M0	
278	297	III	Rectum	4	T3	G2	Invasion into perirectal adipose tissue.	Pos	7/10	N2	Neg	M0	Descending colon polyps, no HGD or carcinoma identified..

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Pt ID	Path ID	Grp	Anatom Loc	Size	Grade	Histo Grade	Local Invasion	Lymph Met	Lymph Met Incid	Reg Lymph Grade	Dist Met & Loc	Dist Met Grade	Comment
295	314	II	Ascending colon	5.0	T3	G2	Invasion through muscularis propria into pericolic adipose tissue.	Neg	0/12	N0	Neg	M0	Melanosis coli and diverticular disease.
296	315	III	Cecum	5.5	T3	G2	Invasion through muscularis propria and invades pericolic adipose tissue. Ileocecal junction.	Pos	2/12	N1	Neg	M0	Tubulovillous adenoma (2.0 cm) with no high grade dysplasia. Neg. liver biopsy.
339	358	II	Rectosigmoid	6	T3	G2	Extends into perirectal fat but does not reach serosa	Neg	0/6	N0	Neg	M0	1 hyperplastic polyp identified
341	360	II	Ascending colon	2 cm invasive	T3	G2	Invasion through muscularis propria to involve pericolonic fat. Arising from villous adenoma.	Neg	0/4	N0	Neg	MX	
356	375	II	Sigmoid	6.5	T3	G2	Through colon wall into subserosal adipose tissue. No serosal spread seen.	Neg	0/4	N0	Neg	M0	
392	444	IV	Ascending colon	2	T3	G2	Invasion through muscularis propria into subserosal adipose tissue, not serosa.	Pos	1/6	N1	Pos - Liver	M1	Tumor arising at prior ileocolic surgical anastomosis.

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393	445	II	Cecum	6.0	T3	G2	Cecum, invades through muscularis propria to involve subserosal adipose tissue but not serosa.	Neg	0/21	N0	Neg	M0	
413	465	IV	Cecum	4.8	T3	G2	Invasive through muscularis to involve periserosal fat; abutting ileocecal junction.	Neg	0/7	N0	Pos - Liver	M1	redagnosis of oophorectomy path to metastatic colon cancer.
505	383	IV		7.5	T3	G2	Invasion through muscularis propria involving pericolic adipose, serosal surface uninvolved	Pos	2/17	N1	Pos - Liver	M1	Anatomical location of primary not notated in report. Evidence of chronic colitis.
517	395	IV	Sigmoid	3	T3	G2	penetrates muscularis propria, involves pericolic fat.	Pos	6/6	N2	Neg	M0	No mention of distant met in report
546	565	IV	Ascending colon	5.5	T3	G2	Invasion through muscularis propria extensively through submucosal and extending to serosa.	Pos	6/12	N2	Pos - Liver	M1	

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577	596	II	Cecum	11.5	T3	G2	Invasion through the bowel wall, into subserosal adipose. Serosal surface free of tumor.	Neg	0/58	N0	Neg	M0	Appendix dilated and fibrotic, but not involved by tumor
695	714	II	Cecum	14.0	T3	G2	extending through bowel wall into serosal fat	Neg	0/22	N0	Neg	MX	moderately differentiated adenocarcinoma with mucinous differentiation (% not stated), tubular adenoma and hyperplastic polyps present,
784	803	IV	Ascending colon	3.5	T3	G3	through muscularis propria into pericolic soft tissues	Pos	5/17	N2	Pos - Liver	M1	invasive poorly differentiated adenosquamous carcinoma
786	805	IV	Descending colon	9.5	T3	G2	through muscularis propria into pericolic fat, but not at serosal surface	Neg	0/12	N0	Pos - Liver	M1	moderately differentiated invasive adenocarcinoma ^a

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Pt ID	Path ID	Grp	Anatom Loc	Size	Grade	Histo Grade	Local Invasion	Lymph Met	Lymph Met Incid	Reg Lymph Grade	Dist Met & Loc	Dist Met Grade	Comment
787	806	II	Rectosigmoid	2.5	T3	G2-G3	Invasion of muscularis propria into soft tissue	Neg		N0	Neg	MX	Peritumoral lymphocytic response; 5 LN examined in pericolic fat, no metastases observed.
789	808	IV	Cecum	5.0	T3	G2-G3	Extending through muscularis propria into pericolic fat	Pos	5/10	N2	Pos - Liver	M1	Three fungating lesions examined.
790	809	IV	Rectum	6.8	T3	G1-G2	Invading through muscularis propria into perirectal fat	Pos	3/13	N1	Pos - Liver	M1	
791	810	IV	Ascending colon	5.8	T3	G3	Through the muscularis propria into pericolic fat	Pos	13/25	N2	Pos - Liver	M1	poorly differentiated invasive colonic adenocarcinoma
801	820	IV				G3		Pos	1/1		Pos-liver	M1	portal lymph node biopsy shows poorly differentiated metastatic adenocarcinoma consistent with colonic primary tumor
802	821	IV						Neg			Pos-liver, 3 foci	M1	
804	823	IV						Neg			Pos-liver	M1	

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805	824	IV						Pos	1/1		Pos-liver	M1	celiac lymph node biopsy shows metastatic adenocarcinoma consistent with colonic primary tumor
806	825	IV				G3		Neg			Pos-liver	M1	
807	826	IV						Neg			Pos-liver	M1	
808	827	IV						Neg			Pos-liver	M1	
809	828	IV						Neg			Pos-liver	M1	
811	830	IV						Neg			Pos-liver	M1	
813	832	IV	Sigmoid	3.0	T3	G2	through muscularis propria into pericolic soft tissue	Pos	7/7	N2	Pos-liver	M1	
814	833	IV						Neg			Pos-liver	M1	
815	834	IV						Neg			Pos-liver	M1	
817	836	IV				G2		Neg			Pos-liver	M1	
818	837	IV				G2		Neg			Pos-liver	M1	
819	838	IV						Neg			Pos-liver	M1	
820	839	IV						Neg			Pos-liver, duodenum	M1	
821	840	IV						Neg			Pos-liver	M1	
822	841	IV				G2		Neg			Pos-liver	M1	

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823	842	IV	Descending colon	5.0	T3	G3	through muscularis propria into perirectal soft tissue	Pos	2/11	N1	Pos-liver	M1	moderately to poorly differentiated primary tumor
826	845	IV						Neg			Pos-liver, diaphragm, gallbladder nodule	M1	
827	846	IV						Neg			Pos-liver, peritoneum	M1	
828	847	IV						Neg			Pos-liver	M1	
829	848	IV						Neg			Pos-liver	M1	moderately to poorly differentiated
830	849	IV				G3		Neg			Pos-liver	M1	moderately to poorly differentiated metastatic tumor
831	850	IV				G2		Neg			Pos-liver	M1	
832	851	IV						Pos	2/2		Pos-liver	M1	
833	852	IV				G2		Neg			Pos-liver	M1	
834	853	IV						Neg			Pos-liver	M1	
835	854	IV						Neg			Pos-liver	M1	
836	855					G2		Neg			Pos-liver	M1	
837	856	IV				G2		Neg			Pos-liver	M1	

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888	908	IV	Ascending colon	2.0	T2	G1	Into muscularis propria	Pos	3/21	N0	Pos - Liver	M1	well to moderately differentiated adenocarcinoma; this patient has tumors of the ascending colon and the sigmoid colon
889	909	IV	Cecum	4.8	T3	G2	Through muscularis propria into subserosal tissue	Pos	1/4	N1	Pos - Liver	M1	moderately differentiated adenocarcinoma
890	910	IV	Ascending colon		T3	G2	Through muscularis propria into subserosa.	Pos	11/15	N2	Pos - Liver	M1	
891	911	IV	Rectum	5.2	T3	G2	Invasion through muscularis propria into perirectal soft tissue	Pos	4/15	N2	Pos - Liver	M1	Perineural invasion present.
892	912	IV	Sigmoid	5.0	T3	G2	Invasion into pericolic sort tissue. Tumor focally invading skeletal muscle attached to colon.	Pos	1/28	N1	Pos - Liver, left and right lobe, omentum	M1	Perineural invasion present, extensive. Patient with a history of colon cancer.

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Pt ID	Path ID	Grp	Anatom Loc	Size	Grade	Histo Grade	Local Invasion	Lymph Met	Lymph Met Incid	Reg Lymph Grade	Dist Met & Loc	Dist Met Grade	Comment
893	913	IV	Transverse colon	6.0	T3	G2-G3	Through muscularis propria into pericolic fat	Pos	14/17	N2	Pos - Liver	M1	Perineural invasion focally present. Omentum mass, but resection with no tumor identified.



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION TBLASTX 2.2.2 [Dec-14-2001]

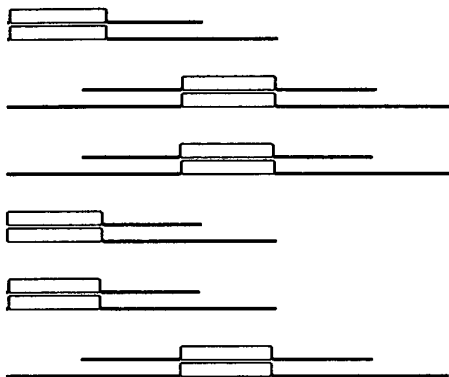
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x_dropoff: expect: wordsize: Filter ☐ Align

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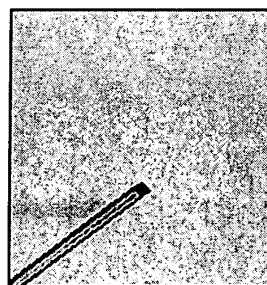
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Sequence 2
2 gi 2156932
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cDNA clone IMAGE:793096 5' similar to TR:G555806
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Length 415 (1 .. 415)



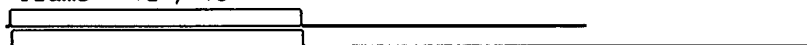
2



1

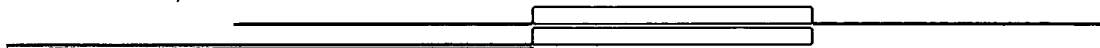
NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 104 bits (222), Expect = 2e-21
Identities = 39/50 (78%)
Frame = +1 / +3



Query: 4 LTLACTPGSSPTLLRWFHDCLGFCFLPLSPGEDPELGLEMTAGFGLGGMR 153
LTLACT GSSP L+RWFHDCLGFLHLPLSPGEDPE+GL++ AG G GG+R
Sbjct: 3 LTLACTSGSSPMLMRWFHDCLGFFHLLPLSPGEDPEMGLKVAAGSGRGGLR 152

Score = 93.2 bits (197), Expect = 6e-18
Identities = 37/48 (77%)
Frame = -1 / -1



Query: 146 PPSNPFAVISRPSSGSSPGLSGKWQKPRQSWNQKSVGELPGVQAKVR 3
PP P+PA RP SGSSPGLSGKW KPRQSWNQ R S+GELP VQAKV+
Sbjct: 145 PPRPDPAATLRPISSGSSPGLSGKW*KPRQSWNQRIISIGELPEVQAKVK 2

Score = 84.5 bits (178), Expect = 3e-15
Identities = 35/48 (72%)
Frame = -3 / -3

Query: 147 SPKPKPCCHFKAQLGIFTWAQRQVAKAQAVVEPAQKCGGAAGGAGQGQ 4
SP P+PC H +A L I TWAQRQV KA AVVEPA K GAAGGAGQGQ 10
Sbjct: 146 SPSRPRCSHLEAHLRILTWAQRQVKA*AVVEPAHKHRGAAGGAGQGQ 3

Score = 81.7 bits (172), Expect = 2e-14
Identities = 35/49 (71%)
Frame = +2 / +1

Query: 2 T*PWPAPPAAPPHFCAGSTTAWAFATCR*AQVKIPSWALK*QQGLGLGE 148
T*PWPAPPAAP CAGSTTA AF TCR*AQV+I WA + QGLG G+ 9
Sbjct: 1 T*PWPAPPAAPLCLCAGSTTA*AFTTCR*AQVRIRRWASRWLQGLGED 147

Score = 73.9 bits (155), Expect = 4e-12
Identities = 33/47 (70%)
Frame = +3 / +2

Query: 6 DLGLHPRQLPHTFALVPRLPGLLPLAAEPR*RSRAGP*NDSRVWAWG 146
DLGLH RQLP+ +ALVPRLP L PLAAEPR* S GP RVWA G 7
Sbjct: 5 DLGLHLRQLPYAYALVPRLPRLSPLAAEPR*GSGDGPQGGCRVWARG 145

Score = 70.3 bits (147), Expect = 5e-11
Identities = 33/47 (70%)
Frame = -2 / -2

Query: 145 PQAQTLISFQGPARDLHLGSAASGKSPGSRGTSKAVWGSCRCRPRS 5
P AQTL GP+ D HLGSAASG+S GSRGTS GSCR CRPRS 8
Sbjct: 144 PLAQTLQPP*GPSPDPLGSAASGESLGSRGTS*A*GSCRRCRPRS 4

CPU time: 0.07 user secs. 0.03 sys. secs 0.10 total secs.

Lambda K H
0.318 0.135 0.401

Matrix: BLOSUM62
Number of Hits to DB: 623
Number of Sequences: 0
Number of extensions: 18
Number of successful extensions: 6
Number of sequences better than 10.0: 1
length of database: 1,668,972,645
effective HSP length: 54
effective length of database: 1,367,552,853
effective search space used: 61539878385
frameshift window, decay const: 50, 0.1
T: 13

A: 40
X1: 16 (7.3 bits)
X2: 109 (49.9 bits)
S1: 41 (21.7 bits)

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BLAST 2 SEQUENCES RESULTS VERSION TBLASTX 2.2.2 [Dec-14-2001]

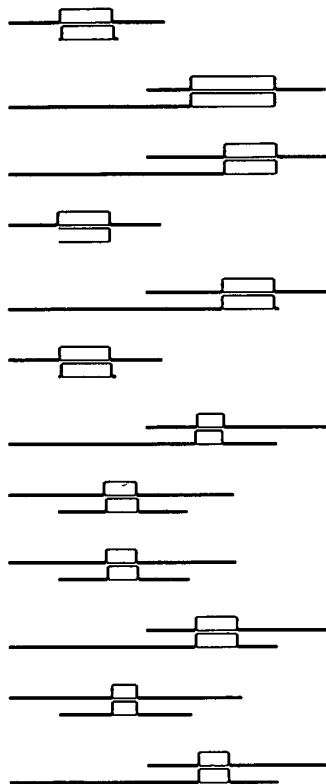
Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☐

Sequence 1
lcl|seq_1

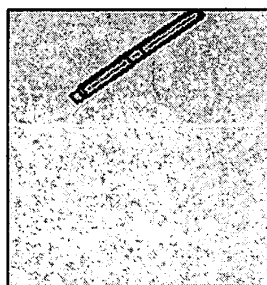
Length 300 (1 .. 300)

Sequence 2
gi 1423522
zd77c01.r1 Soares_fetal_heart_NbHH19W Homo sapiens
cDNA clone IMAGE:346656 5' similar to contains Alu
repetitive element;contains element TAR1 repetitive
element ;.

Length 446 (1 .. 446)



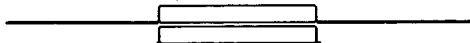
2



1

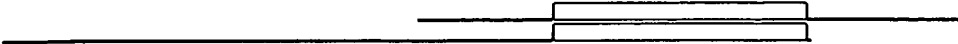
NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 70.7 bits (148), Expect(2) = 2e-18
Identities = 28/29 (96%)
Frame = -1 / -2



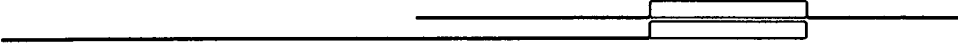
Query: 216 SAHRNLHLLKGF*WQNVSLNAGPRITAPA 130
SAHRNLHLLKGF*WQN+SLNAGPRITAPA
Sbjct: 445 SAHRNLHLLKGF*WQNLSLNAGPRITAPA 359

Score = 70.3 bits (147), Expect = 5e-11
Identities = 32/47 (68%)
Frame = +1 / +2



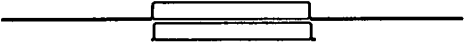
Query: 76 RHEPRLAKGFNELMDVQCWGCYSRACIETHILPSKAF*EVEAVS* 216
RHE K CWGCYSRACIET ILPSKAF*EVEAVS*
Sbjct: 305 RHEHAWPKDLN*WMYSCWGCYSRACIETQILPSKAF*EVEAVS* 445

Score = 70.3 bits (147), Expect(2) = 1e-18
Identities = 28/29 (96%)
Frame = +2 / +3



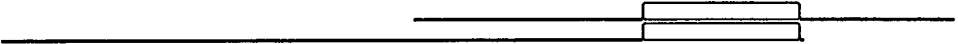
Query: 131 AGAVILGPALRLTFCHQKPFKRWRLR*AD 217
AGAVILGPALRL FCHQKPFKRWRLR*AD
Sbjct: 360 AGAVILGPALRLKFCHQKPFKRWRLR*AD 446

Score = 68.0 bits (142), Expect(2) = 2e-16
Identities = 28/29 (96%)
Frame = -3 / -1




Query: 217 VSSPQPPLKRLMAKCESQCRP*NNSPS 131
VSSPQPPLKRLMAK ESQCRP*NNSPS
Sbjct: 446 VSSPQPPLKRLMAKFESQCRP*NNSPS 360

Score = 64.3 bits (134), Expect(2) = 2e-15
Identities = 27/29 (93%)
Frame = +3 / +1




Query: 129 VLGLLF*GLH*DSHFAIKSLLRGGGCGEL 215
+LGLLF*GLH*DS+FAIKSLLRGGGCGEL
Sbjct: 358 LLGLLF*GLH*DSNFAIKSLLRGGGCGEL 444

Score = 57.9 bits (120), Expect(2) = 1e-12
Identities = 27/28 (96%)
Frame = -2 / -3



Query: 215 QLTATSTS*KAFDGKM*VSMQALE*QPQ 132
QLTATSTS*KAFDGK+*VSMQALE*QPQ
Sbjct: 444 QLTATSTS*KAFDGKI*VSMQALE*QPQ 361

Score = 45.0 bits (92), Expect(2) = 1e-18
Identities = 15/15 (100%)
Frame = +2 / +2



Query: 86 HHAWPKDLMN*WMYS 130
HHAWPKDLMN*WMYS
Sbjct: 314 HHAWPKDLMN*WMYS 358

Score = 44.1 bits (90), Expect(2) = 2e-18
Identities = 16/18 (88%)
Frame = -3 / -2

Query: 139 SPSTVHPLIH*ILWPGVV 86
+P+TVHPLIH*ILWPGVV
Sbjct: 367 APATVHPLIH*ILWPGVV 314

Score = 40.0 bits (81), Expect(2) = 2e-16
Identities = 15/17 (88%)
Frame = -2 / -1

Query: 137 PQHCTSINSLNPLARRG 87
P +CTSINSLNPLARRG
Sbjct: 365 PSNCTSINSLNPLARRG 315

Score = 40.0 bits (81), Expect(2) = 2e-15
Identities = 17/23 (73%)
Frame = +3 / +3

Query: 84 ATTPGQRI**INGCTVLGLLF*G 152
+TTPGQRI**INGCTV G + G
Sbjct: 312 STTPGQRI**INGCTVAGAVILG 380

Score = 37.3 bits (75), Expect(2) = 1e-12
Identities = 14/14 (100%)
Frame = -1 / -3

Query: 129 LYIH*FIKSFGQAW 88
LYIH*FIKSFGQAW
Sbjct: 357 LYIH*FIKSFGQAW 316

Score = 37.3 bits (75), Expect = 0.42
Identities = 15/17 (88%)
Frame = +1 / +1

Query: 88 PRLAKGFNELMDVQCWG 138
PRLAKGFNELMDVQ G
Sbjct: 316 PRLAKGFNELMDVQLLG 366

CPU time: 0.09 user secs. 0.02 sys. secs 0.11 total secs.

Lambda	K	H
0.318	0.135	0.401

Matrix: BLOSUM62
Number of Hits to DB: 581
Number of Sequences: 0
Number of extensions: 24
Number of successful extensions: 12
Number of sequences better than 10.0: 1
length of database: 1,668,972,645
effective HSP length: 54
effective length of database: 1,368,557,577
effective search space used: 61585090965
frameshift window, decay const: 50, 0.1
T: 13
A: 40
X1: 16 (7.3 bits)
X2: 109 (49.9 bits)
S1: 41 (21.7 bits)

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BLAST 2 SEQUENCES RESULTS VERSION TBLASTX 2.2.2 [Dec-14-2001]

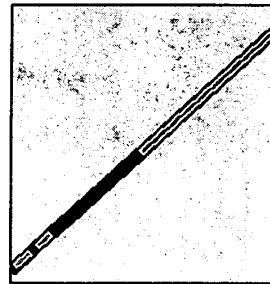
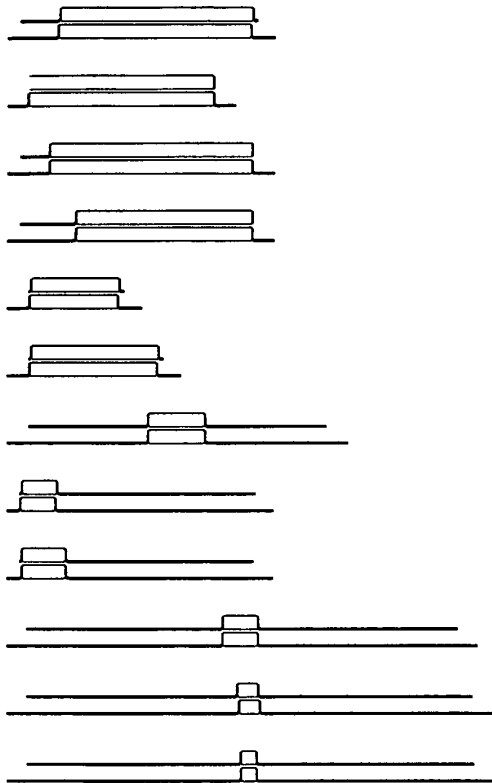
Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☒ Align

Sequence
1 lcl|seq_1

Length 300 (1 .. 300)

Sequence gi me19d10.r1 Soares mouse embryo NbME13.5 14.5 Mus
2 1375806 musculus cDNA clone IMAGE:387955 5'.

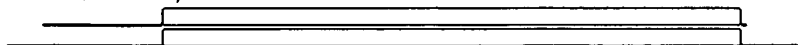
Length 342 (1 .. 342)



1

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 174 bits (375), Expect(2) = 1e-47
Identities = 69/82 (84%)
Frame = +2 / +2



Query: 53 L RSLTRQLVQDENVRGVITMNEEYETRFLCNSSQEWKRLGVEQLRLSTVDMTGIP TL DNL 232
L+++TR+LV DENVRGVITMNEEYETRFLCN+S+EWK+ GVEQLRLSTVDMTG+PTL NL

2 1

Sbjct: 68 LKNMTRRLVLDENVRGVITMNEEYETRFLCNTSKEWKAGVEQLRLSTVDMTGVPPTLANL 247

Query: 233 QKGVQFALKYQSLGQCVYVHCK 298

KGVQFALKYQ+LGQCVYVHCK

Sbjct: 248 HKGVQFALKYQALGQCVYVHCK 313

Score = 166 bits (356), Expect (2) = 6e-42

Identities = 67/79 (84%)

Frame = -1 / -1

Query: 300 ALQCT*THWPSDWYLRANWTPFWRLSKVGIPVMSTVLSRSCSTPSLFHSCEELHRNLVSY 121

ALQCT*THWPS WYLRANWTP WRL+KVG PVMSTVLSRSCSTP+ FHS E LHRN VSY

Sbjct: 315 ALQCT*THWPSAWYLRANWTPLWRLAKVGTPVMSTVLSRSCSTPAFFHSFEVLHRNRVSY 136

Query: 120 SSFMVITPRTFSSCTSWRV 64

SSF+VITPRTFSS TS RV

Sbjct: 135 SSFIVITPRTFSSSTSRV 79

Score = 146 bits (313), Expect (2) = 4e-38

Identities = 59/87 (67%)

Frame = +1 / +1

Query: 40 GALRVAELDAPAGTGRERARGDHHGERVDEVPVQLFTGVEETRSRXXXQHSRHDWDPH 219

G E DAPAGTGRERARGDH+ERGVDR +PVQ G+EE+RS QHSRHDW P+

Sbjct: 55 GRAAAEEHDAPAGTGRERARGDHYERGVDRPIPVQHLEGMEESRS*AATAQHSRHDWGP 234

Query: 220 LGQPPEGSPICSQVPVAGPVCLRAL*G 300

LGQ P+ SP+CSQVP GPVCL AL*G

Sbjct: 235 LGQSPQRSVPVCSQVPGTGPVCLCAL*G 315

Score = 90.4 bits (191), Expect = 4e-17

Identities = 40/75 (53%)

Frame = +3 / +3

Query: 75 WYRTRTCAXXXXXXXXXXXXXCATLHRSGRD*ESXXXXSAQ*T*LGSPPWTTSRRESNLL 254

WY TRTCA CAT R+GR E SAQ T*LGS PW S +ES+LL

Sbjct: 90 WYWTRTCAG*SL*TRSTRPDSCATPRRNGRKQELSSYGSAQST*LGSQPWPISTKESLL 269

Query: 255 SSTSRWASVFTCIVR 299

SST WASV CIVR

Sbjct: 270 SSTRHWASVSMCIVR 314

Score = 70.3 bits (147), Expect (3) = 5e-21

Identities = 28/38 (73%)

Frame = -3 / -3

Query: 298 LTMHVNTLAQRLVLESKLDLSLLEVQGGDP SHVYCAEX 185

LTMH++TLAQ LVLESK LDS +E+ QG DPSHV CAE
Sbjct: 313 LTMHIDTLAQCLVLESK LDSFVEIGQGWDPSHV DCAEP 200

Score = 60.2 bits (125), Expect(2) = 7e-09
Identities = 33/55 (60%)
Frame = -2 / -2

Query: 299 PYNARKHTGPATGT*EQIGLPSGGCPRWGSQXXXXXXXXXXXXLV SSTPVKSCTG 135
PYN A +HTGP GT*EQ GL G PR G QS L+SS P + CTG
Sbjct: 314 PYN AHRHTGPPVPGT*EQTGLLCGDWPRLG PQSRLC*AVAAQLLLSSIPSR CCTG 150

Score = 47.8 bits (98), Expect(3) = 5e-21
Identities = 10/24 (41%)
Frame = -3 / -3

Query: 145 VAQXXXXXXXXXXXXXAHVLVLYQ 74
VAQ AHVLV YQ
Sbjct: 160 VAQESGLVLLVHSDHPAHVLVQYQ 89

Score = 37.7 bits (76), Expect(2) = 1e-47
Identities = 2/15 (13%)
Frame = +1 / +2

Query: 4 DWXXXXXXXXXXXXX 48
DW
Sbjct: 20 DWYHRIDHTVLLGAL 64

Score = 34.1 bits (68), Expect(2) = 4e-38
Identities = 2/19 (10%)
Frame = +2 / +3

Query: 5 TGXXXXXXXXXXXXX 61
TG
Sbjct: 21 TGTTASTTRFCWARCR*RT 77

Score = 27.2 bits (53), Expect(2) = 6e-42
Identities = 2/15 (13%)
Frame = -1 / -3

Query: 48 XXXXXXXXXXXXXPV 4
PV
Sbjct: 64 QRAQQNRVVDAVVPV 20

Score = 22.6 bits (43), Expect(3) = 5e-21
Identities = 3/9 (33%)
Frame = -2 / -1

Query: 29 XXXXXYQS 3
YQS
Sbjct: 45 VWSMRWYQS 19

Score = 21.7 bits (41), Expect(2) = 7e-09
Identities = 2/7 (28%)
Frame = -3 / -2

Query: 25 XXXXTS 5
TS
Sbjct: 41 GRCGGTS 21

CPU time: 0.10 user secs. 0.03 sys. secs 0.13 total secs.

Lambda	K	H
0.318	0.135	0.401

Matrix: BLOSUM62
Number of Hits to DB: 662
Number of Sequences: 0
Number of extensions: 21
Number of successful extensions: 12
Number of sequences better than 10.0: 1
length of database: 1,720,680,694
effective HSP length: 54
effective length of database: 1,410,958,186
effective search space used: 63493118370
frameshift window, decay const: 50, 0.1
T: 13
A: 40
X1: 16 (7.3 bits)
X2: 109 (49.9 bits)
S1: 41 (21.7 bits)



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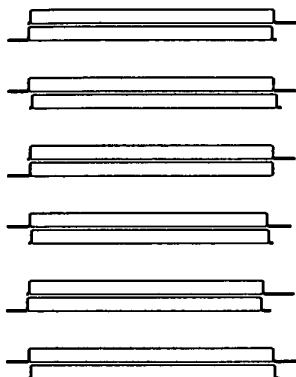
Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☐ Align

Sequence
1 lcl|seq_1

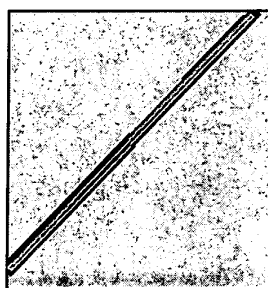
Length 300 (1 .. 300)

Sequence gi mn14a11.r1 Beddington mouse embryonic region Mus
2 1668613 musculus cDNA clone IMAGE:537884 5'.

Length 298 (1 .. 298)



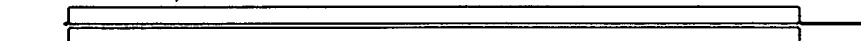
2



1

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 220 bits (474), Expect = 4e-56
Identities = 91/91 (100%)
Frame = +3 / +3

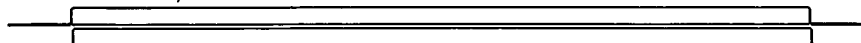


Query: 3 DLCRESDLRHAMANCFEALIGAVYLEGSLEEAKQLFGRLLFNDPDLREVWLNYPHPLQL 182
DLCRESDLRHAMANCFEALIGAVYLEGSLEEAKQLFGRLLFNDPDLREVWLNYPHPLQL
Sbjct: 24 DLCRESDLRHAMANCFEALIGAVYLEGSLEEAKQLFGRLLFNDPDLREVWLNYPHPLQL 203

91

Query: 183 QEPNTDRQLIETSPVLQKLTEFEEAIGVIFT 275
QEPNTDRQLIETSPVLQKLTEFEEAIGVIFT
Sbjct: 204 QEPNTDRQLIETSPVLQKLTEFEEAIGVIFT 296

Score = 202 bits (435), Expect = 9e-51
Identities = 89/92 (96%)
Frame = -3 / -1



Query: 277 *VKITPIASSNSVSFCRTGEVSIICRSVFGSCSWGWRG*LSQTSRRSGSLKSKRPNNCL 98
*VKITPIASSNSVSFCRTGEVSIICRSVFGSCSWGWRG*LSQTSRRSGSLKSKRPNNCL

Sbjct: 298 *VKITPIASSNSVSFCRTGEVSISCRSVFGSCSWSGWRG*LSQTSRRSGSLKSKRPNNCL 119

Query: 97 ASSRLPSK*TAPINASKQLAIACRRSDSLQRS 2

ASSRLPSK*TAPI ASKQLAIA RRSDSL RS

Sbjct: 118 ASSRLPSK*TAPIKASKQLAIAWRRSDSLHRS 23

Score = 157 bits (337), Expect = 3e-37

Identities = 69/91 (75%)

Frame = +2 / +2

Query: 5 PL*RIGPSTCNGQLF*SVNRSCLLGGKPGGSQAVIWTLL**SGPARSLAQLSSPPTPTT 184

P**RI C+GQLF*S++RSCLLGG+P GSQ VIWTL L**SGP+RSLAQLSSPPTPTT

Sbjct: 26 PM*RIRSPPCDQQLF*SLDRSCLLGGEPRGSQTVIWTLL**SGPSRLAQLSSPPTPTT 205

Query: 185 RAKY*STTY*NFSSSTKTY*V*RSNWSNFYS 277

RAKY S TY*NF SST+TY V*RS+WS+ +S

Sbjct: 206 RAKYGSATY*NFPSSTETYGV*RSDWSDLHS 298

Score = 149 bits (321), Expect = 5e-35

Identities = 68/89 (76%)

Frame = -2 / -3

Query: 275 SKNYSNCFKLSKFL*NWRSFNKLSISIWLL*LEWVERIIEPDFAQVRIIKEQASK*LLG 96

S+++SN FFKL KFL*NW SFNKL I IWLL*LEWVERIIEPDF++VRIIKE ASK*L G

Sbjct: 296 SEDHSNRFFKLKFL*NWGSFNKLPIRIWLL*LEWVERIIEPDFSKVRIIKE*ASK*LFG 117

Query: 95 FLQASLQVNSSY*RFKTIGHCMSKVRFST 9

FL A LQVNSSY FKTIGH M+++ FST

Sbjct: 116 FL*APLQVNSSYQGFKTIGHRMAEI*FST 30

Score = 149 bits (320), Expect = 7e-35

Identities = 69/88 (78%)

Frame = +1 / +1

Query: 4 TFVENRTFDMQWPIVLKR**ELFTWREAWRKPSYLDACSLMIRTCAGSGSIILSTHSNY 183

T+VEN+ M+WPIVLK **ELFTWR A RKP+SYLDA SLMIRT KSGSIILSTHSNY

Sbjct: 25 TYVENQISAMRWPIVLKP**ELFTWRGA*RKPNYLDAYSMLIRTFEKGSGSIILSTHSNY 204

Query: 184 KSQILIDNLLKLLQFYKNLLSLKKQLE* 267

KSQI I NLLKL QFY+NL SLKK+LE*

Sbjct: 205 KSQIRIGNLLKLPQFYRNLRSLKKRLE* 288

Score = 146 bits (313), Expect = 6e-34

Identities = 69/92 (75%)

Frame = -1 / -2

Query: 276 E*KLLQLLLQTQ*VFVELEKFQ*VVDQYLALVVGVGGEDN*ARLRAGPDH*RASVQITAW 97

E*+ LQ LLQT *V VEL KFQ*V D YLALVVGVGGEDN*ARL GPDH*R SVQIT W
Sbjct: 297 E*RSLQSLQTP*VSVELGKFQ*VADPYLALVVGVGGEDN*ARLLEGPDH*RVSVQITVW 118

Query: 96 LPPGFPPSKQLLLTLQNNWPLHVEGPILYKGQ 1
LP G PPSKQLL LQNNWP H ILY G+
Sbjct: 117 LPLGSPPSKQLLSRLQNNWPSHGGDLILYIGR 22

CPU time: 0.05 user secs. 0.06 sys. secs 0.11 total secs.

Lambda	K	H
0.318	0.135	0.401

Matrix: BLOSUM62
Number of Hits to DB: 638
Number of Sequences: 0
Number of extensions: 19
Number of successful extensions: 6
Number of sequences better than 10.0: 1
length of database: 1,668,972,645
effective HSP length: 54
effective length of database: 1,368,557,577
effective search space used: 61585090965
frameshift window, decay const: 50, 0.1
T: 13
A: 40
X1: 16 (7.3 bits)
X2: 109 (49.9 bits)
S1: 41 (21.7 bits)

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BLAST 2 SEQUENCES RESULTS VERSION TBLASTX 2.2.2 [Dec-14-2001]

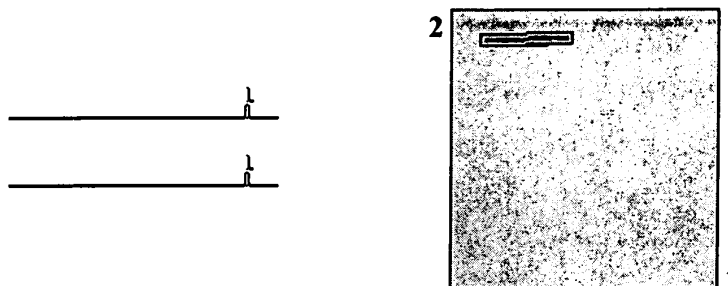
Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☐ Align

Sequence
1 lcl|seq_1

Length 300 (1 .. 300)

Sequence gi Human fibrinogen gamma chain/fibrinogen alpha
2 1117833 chain genes, intergenic region.

Length 13134 (1 .. 13134)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 38.6 bits (78), Expect = 0.16
Identities = 13/22 (59%)
Frame = +1 / +2

Query: 43 Y*L*SPCCTLEKKTYFSCLSKT 108
Y L*SPCCTL+ +TY C+++T
Sbjct: 11663 YQL*SPCCTLDSRTYLYCITQT 11728

Score = 35.9 bits (72), Expect = 1.1
Identities = 15/34 (44%)
Frame = +2 / +3

Query: 35 YKIINYSHHAVPWKRKPTFLA*VKLLPFSRTGGP 136
+ IINYSHHA W + ++A*+KL T P
Sbjct: 11655 HNIINYSHHAHWTPELIYIA*LKLCAL*PTSP 11756

CPU time: 0.06 user secs. 0.03 sys. secs 0.09 total secs.

Lambda K H
0.318 0.135 0.401

Matrix: BLOSUM62

Number of Hits to DB: 11,835
Number of Sequences: 0
Number of extensions: 205
Number of successful extensions: 10
Number of sequences better than 10.0: 1
length of database: 1,668,972,645
effective HSP length: 54
effective length of database: 1,368,557,577
effective search space used: 61585090965
frameshift window, decay const: 50, 0.1
T: 13
A: 40
X1: 16 (7.3 bits)
X2: 109 (49.9 bits)
S1: 41 (21.7 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION TBLASTX 2.2.2 [Dec-14-2001]

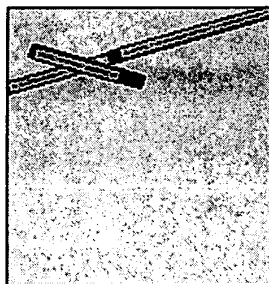
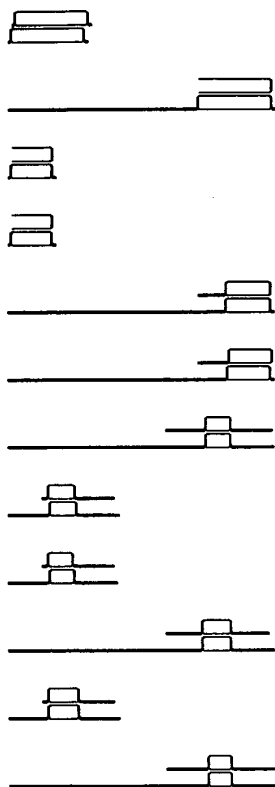
Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☐

Sequence
1 lcl|seq_1

Length 209 (1 .. 209)

Sequence gi Human XP1PO ribosomal protein S3 (rpS3) mRNA,
2 555940 complete cds.

Length 754 (1 .. 754)



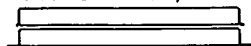
1

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 108 bits (231), Expect = 5e-23

Identities = 44/69 (63%)

Frame = -3 / -3



Query: 207 RRTC YAVGTGWGMAEGSGFPPFCSEMGVVGSISSMGSTMPWDPTGNRGPKKPLPDH VSI 28
RR CYAVGTGWGMA GSGFPPFCSEMGVVGSISS+GSTM+ W G GP P+ S+ 19

Sbjct: 743 RRPCYAVGTGWGMAGGSGFPPFCSEMGVVGSISSLGSTMLTWSGRGFLGPILPVGSQGS 564

Query: 27 VVRLALRSP 1

+ L +P

Sbjct: 563 IFTLMPSTP 537

Score = 101 bits (215), Expect = 7e-21

Identities = 45/69 (65%)

Frame = +2 / +1

Query: 2 GLLRANLTMTLWSGRGFLGPLLPVGSQGIIVEPIDEILPTTPISEQGGKPEPSAMPQP 181

G+L + ML W G +GP P+ IVEP DEILPTTPISEQGGKPEP AMPQP

Sbjct: 538 GVLGIVKIMLPWDPTGKIGPKPLPDHVSIVEPKDEILPTTPISEQGGKPEPPAMPQP 717

Query: 182 VPTA*QVLL 208

VPTA*Q LL

Sbjct: 718 VPTA*QGLL 744

Score = 100 bits (213), Expect = 1e-20

Identities = 36/39 (92%)

Frame = -1 / -1

Query: 209 QGEPVMLWELAGAWQKALASHPSVLRWGWAVSHLWVPQ 93

QG+PVMLW LAGAWQ ALASHPSVLRWGWAVSHLWVPQ

Sbjct: 745 QGDPVMLWGLAGAWQAALASHPSVLRWGWAVSHLWVPQ 629

Score = 100 bits (213), Expect = 1e-20

Identities = 36/39 (92%)

Frame = -2 / -2

Query: 208 KENLLCCGNWLGHGRRLLWPTLLF*DGGGGQYLIYGFHN 92

KE LLCCG+WLGHGRRLLWPTLLF*DGGGGQYLI+GFHN

Sbjct: 744 KETLLCCGDWLGHGRRLLWPTLLF*DGGGGQYLIFGFHN 628

Score = 99.1 bits (210), Expect = 4e-20

Identities = 37/42 (88%)

Frame = +1 / +3

Query: 82 PGHHCCTHR*DTAHHPLRTEGWEARAFCHAPASSHSITGSP 207

P HCGT R*DTAHHPLRTEGWEARA CHAPAS HSITGSP

Sbjct: 618 PREHCGTQR*DTAHHPLRTEGWEARAACHAPASPHSITGSP 743

Score = 93.2 bits (197), Expect = 2e-18

Identities = 35/40 (87%)

Frame = +3 / +2

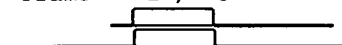
Query: 90 SLWNP*MYCPPPPSQNRRVGSQSLPCPSQFPQHNRFSL 209
+LWNP MRYCPPPPSQNRRVGSQS LPCPSQ PQHNR SL
Sbjct: 626 ALWNPKMRYCPPPPSQNRRVGSQSRLPCPSQSPQHNRVSL 745

Score = 56.5 bits (117), Expect = 2e-07
Identities = 20/23 (86%)
Frame = -3 / +1



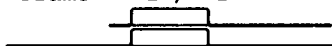
Query: 93 MMPWDPTGNRGPKKPLPDHVSIV 25
M+PWDPTG GPKKPLPDHVSIV
Sbjct: 565 MLPWDPTGKIGPKKPLPDHVSIV 633

Score = 55.6 bits (115), Expect = 5e-07
Identities = 20/25 (80%)
Frame = +2 / -3



Query: 23 TTMLTWSGRGFLGPLLPVGSQGIIV 97
+TMLTWSGRGFLGP+LPVGSQG ++
Sbjct: 635 STMLTWSGRGFLGPILPVGSQGSMI 561

Score = 55.1 bits (114), Expect = 6e-07
Identities = 20/24 (83%)
Frame = +1 / -2



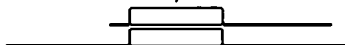
Query: 22 YHNAHVVRQGLLRAPVTSWVPGHH 93
+HNAHVVRQGLLRA +TSWVPG H
Sbjct: 636 FHNAHVVRQGLLRANLTSWVPGQH 565

Score = 51.9 bits (107), Expect = 6e-06
Identities = 21/27 (77%)
Frame = -2 / +3



Query: 103 GFHNDALGPNW*QGP*EAPA*PREHCG 23
G + ALGPNW* P*EAPA*PREHCG
Sbjct: 555 GEDHAALGPNW*DWP*EAPA*PREHCG 635

Score = 51.5 bits (106), Expect = 8e-06
Identities = 22/29 (75%)
Frame = +3 / -1



Query: 21 LPQCSRGQAGAS*GPCYQLGPRASLWNP* 107
+PQCSRGQAGAS*G YQLGPRA+ +P*
Sbjct: 637 VPQCSRGQAGAS*GQSYQLGPRAA*SSP* 551

Score = 49.6 bits (102), Expect = 3e-05
Identities = 20/22 (90%)
Frame = -1 / +2



Query: 89 CPGTQLVTGALRSPCLTT*ALW 24
CPGTQLV ALRSPCLTT*ALW
Sbjct: 569 CPGTQLVRLALRSPCLTT*ALW 634

CPU time: 0.10 user secs. 0.01 sys. secs 0.11 total secs.

Lambda	K	H
0.318	0.135	0.401

Matrix: BLOSUM62
Number of Hits to DB: 1171
Number of Sequences: 0
Number of extensions: 38
Number of successful extensions: 20
Number of sequences better than 10.0: 1
length of database: 1,668,972,645
effective HSP length: 51
effective length of database: 1,261,711,380
effective search space used: 22710804840
frameshift window, decay const: 50, 0.1
T: 13
A: 40
X1: 16 (7.3 bits)
X2: 109 (49.9 bits)
S1: 41 (21.7 bits)

**Blast 2 S quences results**

PubMed

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Taxonomy

Structure

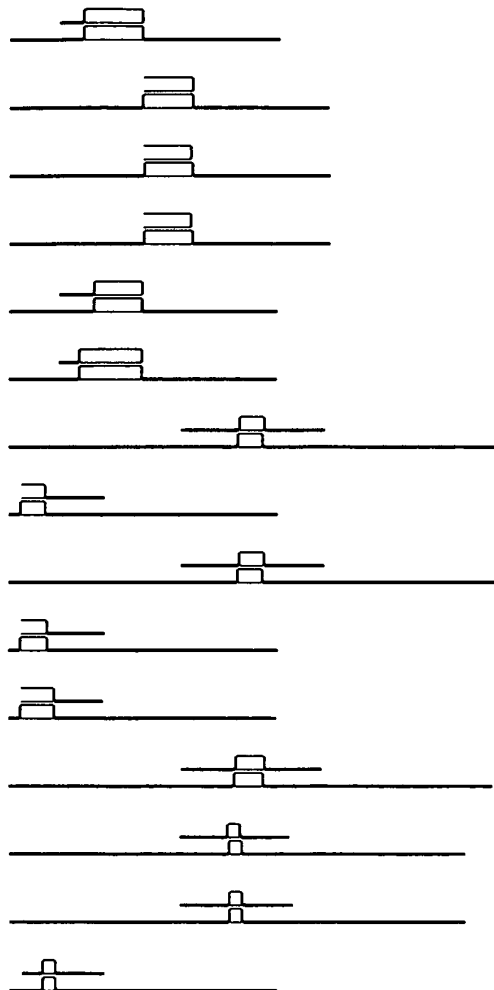
BLAST 2 SEQUENCES RESULTS VERSION TBLASTX 2.2.2 [Dec-14-2001]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☐

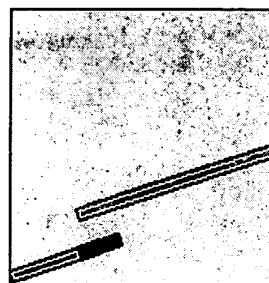
Sequence 1 lcl|seq_1

Length 300 (1 .. 300)

Sequence 2 gi 397648 Mus musculus B6D2F1 clone 2C#4 mRNA. Length 962 (1 .. 962)



2



1

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 154 bits (330), Expect = 1e-35
Identities = 58/70 (82%)
Frame = +2 / +1



Query: 89 ERDKNQSSSKRKVEQFWRFYSHMVRPGDLTGHSDFHLFKEGIKPMWEDDANKNGGKWIIR 268
E++ Q + VEQFW+FYSHMVRPGDLTGHSDFHLFKEGIKPMWEDD NKNGGKWIIR
Sbjct: 268 EQNIKQIGTFPSVEQFWKFYSHMVRPGDLTGHSDFHLFKEGIKPMWEDDPNKNGGKWIIR 447

31

Query: 269 LRKGLASRCW 298
LRKGLASRCW
Sbjct: 448 LRKGLASRCW 477

Score = 133 bits (286), Expect = 3e-30
Identities = 54/59 (91%)
Frame = -1 / -1

Query: 300 SQQREAKPFRSRIIHLPPFLFASSSHMGLIPSLKRWKS LWPVRSPGRTMWL*NLQNCST 124
SQQREAKPFRSR+IHLPPFLF SSSH+GLIPSLKR KSLWPVRSPGRTMWL*N QNCST
Sbjct: 479 SQQREAKPFRSRMIHLPPFLFGSSSHIGLIPSLKR*KSLWPVRSPGRTMWL*NFQNCST 303

Score = 112 bits (240), Expect = 7e-24
Identities = 47/58 (81%)
Frame = -2 / -2

Query: 299 PSNGRPSPSAE*STCHHFYLHHPPTWV*FLL*RDGSHCGLSGPQDVPCGYKTSRTAP 126
PS+G+ SPS E*STC HFYL HPPT V* LL*RD SHCGLSGPQDVPCG KTSRTAP
Sbjct: 478 PSSGKLSPSGVE*STCPHFYLDHPPT*V*SLL*RDESHCGLSGPQDVPCGCKTSRTAP 305

Score = 110 bits (234), Expect = 5e-23
Identities = 45/58 (77%)
Frame = -3 / -3

Query: 298 PATGGQALPQNNPLATIFICIILPHGFNSFFEEMVTVACQVPRTYHVAIKPELLH 125
PA G ALP+ N+PLA IFI IILPH FN FFEEM+VTVACQVPRTYHVA+K PELLH
Sbjct: 477 PAAGS*ALPESNDPLAPIFIWIILPHRFNPFEEEMKVTVACQVPRTYHVAVKLPELLH 304

Score = 109 bits (232), Expect = 9e-23
Identities = 47/58 (81%)
Frame = +1 / +3

Query: 127 GAVLEVL*PHGTSWGPDRPQ*LPSLQRRN*THVGG*CK*KWWQVDYSAEGLGLPLL 300
GAVLEVL PHGTSWGPDRPQ*L SLQRR+*T+VGG* K*KW QVD+S EGL PLLG
Sbjct: 306 GAVLEVLQPHGTSWGPDRPQ*LSSLQRRD*TYVGG*SK*KWGQVDHSTPEGLSFPLL 479


Score = 102 bits (217), Expect(2) = 3e-33
Identities = 48/74 (64%)
Frame = +3 / +2

Query: 78 RKKRNETRIRAVARERWSSSGGFATWYVLGT*QATVTSISSKKELNPCGRMMQIKMVAS 257

R+ + T R WSSSG F ATWYVLGT*QATVT ISSKK LN CGRM+QIKM AS
Sbjct: 257 RRAMRTSSRLAPFPLWSSSGSFTATWYVLGT*QATVTFISSKKGLNLCGRMIQIKMGAS 436


Query: 258 GLFGCGRAWPPVAG 299
G F GRA P AG
Sbjct: 437 GSFDSGRA*LPAAG 478

Score = 74.4 bits (156), Expect(2) = 6e-14
Identities = 26/30 (86%)
Frame = -2 / -3



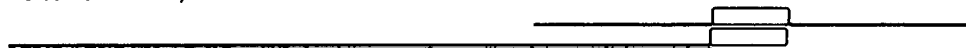
Query: 92 VPFFPSHHLSVCCFLHSDHGPHCHHLSKRR 3
V FFPSHHLSVCCFLHSDHG HCHHL +RR
Sbjct: 135 VLFFPSHHLSVCCFLHSDHGLHCHHLLRRR 46

Score = 74.4 bits (156), Expect(2) = 1e-12
Identities = 29/29 (100%)
Frame = +2 / +3




Query: 2 FDALKDDSGDHDQNEENSTQKDGEKEKT 88
FDALKDDSGDHDQNEENSTQKDGEKEKT
Sbjct: 45 FDALKDDSGDHDQNEENSTQKDGEKEKT 131

Score = 70.3 bits (147), Expect(2) = 7e-12
Identities = 29/30 (96%)
Frame = -1 / -2




Query: 90 SVFSFSPSFCVLFSSF*SWSPLSSSFKASN 1
+VFSFSPSFCVLFSSF*SWSPLSSSFKASN
Sbjct: 133 TVFSFSPSFCVLFSSF*SWSPLSSSFKASN 44

Score = 62.9 bits (131), Expect(2) = 3e-33
Identities = 27/31 (87%)
Frame = +1 / +2



Query: 1 VRRFER**QWGP*SE*RKQHTERW*EGKNGT 93
VRR +R**QW P*SE*RKQHTERW*EGKN T
Sbjct: 44 VRR LKR**QWRP*SE*RKQHTERW*EGKNST 136

Score = 58.3 bits (121), Expect = 2e-07
Identities = 26/41 (63%)
Frame = +3 / +1



Query: 3 STL*KMMTVGTMIRMKKT AHRKMVRRKKRNETRIRAVARER 125
ST *KMMTV TMIRMKKT AHRKMVRRKK+ + + + +
Sbjct: 46 STP*KMMTVETMIRMKKT AHRKMVRRKKQYRDKSQSSGKRK 168

Score = 57.4 bits (119), Expect = 4e-07
Identities = 26/34 (76%)
Frame = -3 / -1

Query: 103 ILVSFRFFLLTIFLCAVFFILIMVPTVIIFQSVE 2
+L + FLLTIFLCAVFFILIMV TVIIF VE
Sbjct: 146 LLSRYCFLLTIFLCAVFFILIMVSTVIIF*GVE 45

Score = 25.8 bits (50), Expect(2) = 6e-14
Identities = 9/15 (60%)
Frame = -2 / -2

Query: 125 PFSCYCSDSLVPFF 81
P SC+CS SCL F
Sbjct: 169 PSSCHCSGSLGTVF 125

Score = 23.1 bits (44), Expect(2) = 7e-12
Identities = 11/15 (73%)
Frame = -3 / -3

Query: 124 LSLATALILVSFRFF 80
L LATAL LVS FF
Sbjct: 168 LPLATALALVSVLFF 124

Score = 22.6 bits (43), Expect(2) = 1e-12
Identities = 10/15 (66%)
Frame = +3 / +2

Query: 81 KKRNETRIRAVARER 125
K ETR RAVAR R
Sbjct: 125 KNSTETRARAVARGR 169

CPU time: 0.09 user secs. 0.03 sys. secs 0.12 total secs.

Lambda	K	H
0.318	0.135	0.401

Matrix: BLOSUM62
Number of Hits to DB: 1323
Number of Sequences: 0
Number of extensions: 37
Number of successful extensions: 16
Number of sequences better than 10.0: 1
length of database: 1,668,972,645
effective HSP length: 54
effective length of database: 1,368,557,577
effective search space used: 61585090965
frameshift window, decay const: 50, 0.1

T: 13
A: 40
X1: 16 (7.3 bits)
X2: 109 (49.9 bits)
S1: 41 (21.7 bits)